

#5

#5



## SEQUENCE LISTING

&lt;110&gt; Klein, Robert

<120> TRANSGENIC MICE CONTAINING LPR5 GENE  
DISRUPTIONS

&lt;130&gt; R-193

&lt;140&gt; US 09/887,540

&lt;141&gt; 2001-06-21

&lt;150&gt; US 60/213,201

&lt;151&gt; 2000-06-21

&lt;150&gt; US 60/223,123

&lt;151&gt; 2000-08-07

&lt;160&gt; 4

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 5119

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 1

gccgaggcgc	ccgaggcggg	agcaagaggg	gccgggagcc	gcgaggatcc	accgccgccg	60
cgcgcgccat	ggagcccag	tgagcgcgcg	gcgctcccgg	ccgccggacg	acatggaaac	120
ggcgccgacc	cgggcccctc	cgccgcgcgc	gccgcgcgtg	ctgctgctgg	tgctgtactg	180
cagcttggtc	cccgcgcggg	cctcaccgct	cctgtgtgtt	gccaacgcgc	gggatgtgcg	240
gctagtggat	gccggcgagg	tgaagctgga	gtccaccatt	gtggccagtg	gcctggagga	300
tgcagctgct	gtagacttcc	agttctccaa	gggtgctgtg	tactggacag	atgtgagcga	360
ggaggccatc	aaacagacct	acctgaacca	gactggagct	gctgcacaga	acattgtcat	420
ctcgggcctc	gtgtcacctg	atggcctggc	ctgtgactgg	gttggcaaga	agctgtactg	480
gacggactcc	gagaccaacc	gcattgaggt	tgccaacctc	aatgggacgt	ccgtaaggt	540
tctcttctgg	caggacctgg	accagccaag	ggccattgcc	ctggatcctg	cacatgggta	600
catgtactgg	actgactggg	gggaagcacc	ccggatcgag	cgggcaggga	tggatggcag	660
taccgggaag	atcattgtag	actccgacat	ttactggccc	aatgggctga	ccatcgacct	720
ggaggaacag	aagctgtact	gggccgatgc	caagctcagc	ttcatccacc	gtgccaacct	780
ggacggctcc	ttccggcaga	aggtgggtgga	gggcagcctc	actcaccctt	ttgccctgac	840
actctctggg	gacacactct	actggacaga	ctggcagacc	cgctccatcc	acgcctgcaa	900
caagtggaca	ggggagcaga	ggaaggagat	ccttagtgct	ctgtactcac	ccatggacat	960
ccaagtgtct	agccaggagc	ggcagcctcc	cttccacaca	ccatgcgagg	aggacaacgg	1020
tggctgttcc	cacctgtgcc	tgtgttcccc	gagggagcct	ttctactcct	gtgcctgccc	1080
cactggtgtg	cagttgcagg	acaatggcaa	gacgtgcaag	acaggggctg	aggaagtgtc	1140
gctgctggct	cggaggacag	acctgaggag	gatctctctg	gacacccttg	acttcacaga	1200
catagtgtct	caggtgggcg	acatccggca	tgccattgcc	attgactacg	atcccttggg	1260
gggctacgtg	tactggaccg	atgatgaggt	gcgggctatc	cgcagggcgt	acctagatgg	1320
ctcaggtgct	cagacacttg	tgaacactga	gatcaatgac	cccgatggca	ttgctgtgga	1380
ctgggtcgcc	cggaaacctct	actggacaga	tacaggcact	gacagaattg	aggtgactcg	1440
cctcaacggc	acctcccga	agatcctggt	atctgaggac	ctggacgaac	cgcgagccat	1500
tgtgttgcac	cctgtgatgg	gcctcatgta	ctggacagac	tggggggaga	accccaaaat	1560
ggaatgcgcc	aacctagatg	ggagagatcg	gcatgtctct	gtgaacacct	cccttgggtg	1620
gccaatgga	ctggccctgg	acctgcagga	gggcaagctg	tactgggggg	atgccaaaac	1680
tgataaaatc	gaggtgatca	acatagacgg	gacaaaagcg	aagaccctgc	ttgaggacaa	1740
gctcccacac	atttttgggt	tcacactgct	gggggacttc	atctactgga	ccgactggca	1800
gagacgcagt	attgaaaggg	tccacaaggt	caaggccagc	cgggatgtca	tcattgatca	1860
actccccgac	ctgatgggac	tcaaagccgt	gaatgtggcc	aaggttgtcg	gaaccaaccc	1920

COPY OF PAPERS  
ORIGINALLY FILED

atgtgaggat	ggaaatggag	ggtgcagcca	tctgtgcttc	ttcacccac	gtgccacca	1980
gtgtggctgc	cccattggcc	tggagctgtt	gagtgacatg	aagacctgca	taatccccga	2040
ggccttcctg	gtattcacca	gcagagccac	catccacagg	atctccctgg	agactaaca	2100
caacgatgtg	gctatccac	tcacgggtgt	caaagaggcc	tctgcactgg	actttgatgt	2160
gtccaacaat	cacatctact	ggactgatgt	tagcctcaag	acgatcagcc	gagccttcat	2220
gaatgggagc	tcagtggagc	acgtgattga	gtttggcctc	gactaccctg	aaggaatggc	2280
tgtggactgg	atgggcaaga	acctctattg	ggcggacaca	gggaccaaca	ggattgaggt	2340
ggcccgjctg	gatgggcagt	tccggcaggt	gcttgtgtgg	agagaccttg	acaacccag	2400
gtctctggct	ctggatccta	ctaaaggcta	catctactgg	actgagtggg	gtggcaagcc	2460
aaggattgtg	cgggccttca	tggatgggac	caattgtatg	acactggtag	acaaggtggg	2520
ccggggccaac	gacctcacca	ttgattatgc	cgaccagcga	ctgtactgga	ctgacctgga	2580
caccaacatg	attgagtctt	ccaacatgct	gggtcaggag	cgcatggtga	tagctgacga	2640
tctgccctac	ccgtttggcc	tgactcaata	tagcgattac	atctactgga	ctgactggaa	2700
cctgcatagc	attgaacggg	cggacaagac	cagtgggagg	aaccgcaccc	tcattccagg	2760
tcacctggac	ttcgtcatgg	acatcctggt	gttccactcc	tcccgtcagg	atggcctcaa	2820
cgactcgctg	cacagcaatg	gccagtgtgg	gcagctgtgc	ctcgccatcc	ccggaggcca	2880
ccgtctgtgg	tgtgctttac	actacacgct	ggaccccgag	agccgcaact	gcagcccgcc	2940
ctccaccttc	ttgctgttca	gccagaaatt	tgccatcagc	cggatgatcc	ccgatgacca	3000
gctcagcccg	gacctgttcc	taccctttca	tgggtgagg	aacgtcaaag	ccatcaacta	3060
tgacccgctg	gacaagttca	tctactgggt	ggacggggcg	cagaacatca	agagggccaa	3120
ggacgacggt	accagccct	ccatgctgac	ctctcccagc	caaagcctga	gccagacag	3180
acagccacac	gacctcagca	ttgacatcta	cagccggaca	ctgttctgga	cctgtgaggc	3240
acccaacact	atcaatgtcc	accggctgga	tggggatgcc	atgggagtgg	tgcttcgagg	3300
ggaccgtgac	aagccaagg	ccattgctgt	caatgctgag	cgaggggtaca	tgtactttac	3360
caacatgcag	gaccatgctg	ccaagatcga	gcgagcctcc	ctggatggca	cagagcgagg	3420
ggtcctcttc	accacaggcc	tcatecgtcc	cgtggccctt	gtggtggaca	atgctctggg	3480
caagctcttc	tgggtggatg	ccgacctaaa	gcgaatcgaa	agctgtgacc	tctctggggc	3540
caaccgcctg	accctggaag	atgccaacat	cgtacagcca	gtaggctctga	cagtgtctgg	3600
caggcacctc	tactggatcg	accgccagca	gcagatgatc	gagcgcgtgg	agaagaccac	3660
tggggacaag	cggactaggg	ttcagggccg	tgtaacccac	ctgacaggca	tccatgccgt	3720
ggaggaagtc	agcctggagg	agttctcagc	ccatccttgt	gcccagagaca	atggcggtcg	3780
ctccacatc	tgtatcgcca	agggtgatgg	aacaccgcgc	tgctcgtgcc	ctgtccacct	3840
ggtgctcctg	cagaacctgc	tgacttgtgg	tgagcctcct	acctgtctcc	ctgatcagtt	3900
tgcatgtacc	actggtgaga	tcgactgcat	cccgggagcc	tggcgctgtg	acggcttccc	3960
tgagtgtgct	gaccagagtg	atgaagaagg	ctgcccagtg	tgctccgcct	ctcagttccc	4020
ctgcgctcga	ggccagtgtg	tggacctgcg	gttacgctgc	gacggtgagg	ccgactgcc	4080
ggatcgctct	gatgaagcta	actgcgatgc	tgtctgtctg	cccaatcagt	tccggtgcac	4140
cagcggccag	tgtgtcctca	tcaagcaaca	gtgtgactcc	ttcccgcact	gtgctgatgg	4200
gtctgatgag	ctcatgtgtg	aaatcaacaa	gccaccctct	gatgacatcc	cagccacag	4260
cagtgccatt	gggcccgtca	ttggtatcat	cctctccctc	ttcgtcatgg	gcgggggtcta	4320
ctttgtctgc	cagcgtgtga	tgtgccagcg	ctacacaggg	gccagtgggc	cctttcccca	4380
cgagtatgtt	ggtggagccc	ctcatgtgcc	tctcaacttc	atagccccag	gtggctcaca	4440
gcacggctcc	ttcccaggca	tcccgtgcag	caagtccgtg	atgagctcca	tgagcctggt	4500
ggggggggcg	ggcagcgtgc	ccctctatga	ccggaatcac	gtcactgggg	cctcatccag	4560
cagctcgtcc	agcacaagg	ccacactata	tccgcgatc	ctgaaccac	ccccgtcccc	4620
ggccacagac	ccctctctct	acaacgtgga	cgtgttttat	tcttcaggca	tcccggccac	4680
cgctagacca	tacaggccct	acgtcattcg	aggatgtgga	cccccaacaa	caccgtgcag	4740
cacagatgtg	tgtgacagtg	actacagcat	cagtcgctgg	aagagcagca	aatactacct	4800
ggacttgaat	tccgactcag	acccctaccc	ccccccgccc	acccccca	gccagtacct	4860
atctgcagag	gacagctgcc	caccctcacc	aggcactgag	aggagtact	gccacctctt	4920
ccgcccccca	ccgtccccct	gcacggactc	gtcctgacct	cggccgtcca	ccggccctcg	4980
ctgcctccct	gtaaatat	ttaaatatga	acaaaggaaa	aatatat	atgatttaaa	5040
aaataaatat	aattgggggt	tttaacaagt	gagaaatgtg	agcgggtgaag	gggtggggcag	5100
ggctgggaaa	cttttctag					5119

<210> 2  
 <211> 1614  
 <212> PRT  
 <213> Mus musculus

<400> 2

Met	Glu	Thr	Ala	Pro	Thr	Arg	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Leu
1				5					10				15	
Leu	Leu	Leu	Val	Leu	Tyr	Cys	Ser	Leu	Val	Pro	Ala	Ala	Ala	Pro
			20					25				30		
Leu	Leu	Leu	Phe	Ala	Asn	Arg	Arg	Asp	Val	Arg	Leu	Val	Asp	Gly
		35				40					45			
Gly	Val	Lys	Leu	Glu	Ser	Thr	Ile	Val	Ala	Ser	Gly	Leu	Glu	Ala
50					55					60				
Ala	Ala	Val	Asp	Phe	Gln	Phe	Ser	Lys	Gly	Ala	Val	Tyr	Trp	Thr
65				70					75					80
Val	Ser	Glu	Glu	Ala	Ile	Lys	Gln	Thr	Tyr	Leu	Asn	Gln	Thr	Gly
				85				90					95	
Ala	Ala	Gln	Asn	Ile	Val	Ile	Ser	Gly	Leu	Val	Ser	Pro	Asp	Gly
			100					105				110		Leu
Ala	Cys	Asp	Trp	Val	Gly	Lys	Lys	Leu	Tyr	Trp	Thr	Asp	Ser	Glu
		115				120						125		Thr
Asn	Arg	Ile	Glu	Val	Ala	Asn	Leu	Asn	Gly	Thr	Ser	Arg	Lys	Val
130						135					140			Leu
Phe	Trp	Gln	Asp	Leu	Asp	Gln	Pro	Arg	Ala	Ile	Ala	Leu	Asp	Pro
145				150					155					Ala
His	Gly	Tyr	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Glu	Ala	Pro	Arg	Ile
			165					170					175	Glu
Arg	Ala	Gly	Met	Asp	Gly	Ser	Thr	Arg	Lys	Ile	Ile	Val	Asp	Ser
		180						185				190		Asp
Ile	Tyr	Trp	Pro	Asn	Gly	Leu	Thr	Ile	Asp	Leu	Glu	Glu	Gln	Lys
	195					200					205			Leu
Tyr	Trp	Ala	Asp	Ala	Lys	Leu	Ser	Phe	Ile	His	Arg	Ala	Asn	Leu
	210				215						220			Asp
Gly	Ser	Phe	Arg	Gln	Lys	Val	Val	Glu	Gly	Ser	Leu	Thr	His	Pro
225				230					235					Phe
Ala	Leu	Thr	Leu	Ser	Gly	Asp	Thr	Leu	Tyr	Trp	Thr	Asp	Trp	Gln
			245					250					255	Thr
Arg	Ser	Ile	His	Ala	Cys	Asn	Lys	Trp	Thr	Gly	Glu	Gln	Arg	Lys
		260						265				270		Glu
Ile	Leu	Ser	Ala	Leu	Tyr	Ser	Pro	Met	Asp	Ile	Gln	Val	Leu	Ser
	275					280					285			Gln
Glu	Arg	Gln	Pro	Pro	Phe	His	Thr	Pro	Cys	Glu	Glu	Asp	Asn	Gly
	290					295					300			Gly
Cys	Ser	His	Leu	Cys	Leu	Leu	Ser	Pro	Arg	Glu	Pro	Phe	Tyr	Ser
305				310					315					Cys
Ala	Cys	Pro	Thr	Gly	Val	Gln	Leu	Gln	Asp	Asn	Gly	Lys	Thr	Cys
			325						330				335	Lys
Thr	Gly	Ala	Glu	Glu	Val	Leu	Leu	Leu	Ala	Arg	Arg	Thr	Asp	Leu
		340						345					350	Arg
Arg	Ile	Ser	Leu	Asp	Thr	Pro	Asp	Phe	Thr	Asp	Ile	Val	Leu	Gln
		355					360				365			Val
Gly	Asp	Ile	Arg	His	Ala	Ile	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Glu
	370				375					380				Gly
Tyr	Val	Tyr	Trp	Thr	Asp	Asp	Glu	Val	Arg	Ala	Ile	Arg	Arg	Ala
385				390					395					Tyr
Leu	Asp	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Val	Asn	Thr	Glu	Ile	Asn
			405					410					415	Asp
Pro	Asp	Gly	Ile	Ala	Val	Asp	Trp	Val	Ala	Arg	Asn	Leu	Tyr	Trp
		420						425				430		Thr
Asp	Thr	Gly	Thr	Asp	Arg	Ile	Glu	Val	Thr	Arg	Leu	Asn	Gly	Thr
		435				440					445			Ser
Arg	Lys	Ile	Leu	Val	Ser	Glu	Asp	Leu	Asp	Glu	Pro	Arg	Ala	Ile
	450					455				460				Val
Leu	His	Pro	Val	Met	Gly	Leu	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Glu
465				470					475				480	Asn
Pro	Lys	Ile	Glu	Cys	Ala	Asn	Leu	Asp	Gly	Arg	Asp	Arg	His	Val
														Leu

				485					490					495			
Val	Asn	Thr	Ser	Leu	Gly	Trp	Pro	Asn	Gly	Leu	Ala	Leu	Asp	Leu	Gln		
			500					505					510				
Glu	Gly	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Lys	Thr	Asp	Lys	Ile	Glu	Val		
		515					520					525					
Ile	Asn	Ile	Asp	Gly	Thr	Lys	Arg	Lys	Thr	Leu	Leu	Glu	Asp	Lys	Leu		
	530					535					540						
Pro	His	Ile	Phe	Gly	Phe	Thr	Leu	Leu	Gly	Asp	Phe	Ile	Tyr	Trp	Thr		
545				550					555						560		
Asp	Trp	Gln	Arg	Arg	Ser	Ile	Glu	Arg	Val	His	Lys	Val	Lys	Ala	Ser		
			565						570					575			
Arg	Asp	Val	Ile	Ile	Asp	Gln	Leu	Pro	Asp	Leu	Met	Gly	Leu	Lys	Ala		
			580					585					590				
Val	Asn	Val	Ala	Lys	Val	Val	Gly	Thr	Asn	Pro	Cys	Ala	Asp	Gly	Asn		
		595					600					605					
Gly	Gly	Cys	Ser	His	Leu	Cys	Phe	Phe	Thr	Pro	Arg	Ala	Thr	Lys	Cys		
	610					615					620						
Gly	Cys	Pro	Ile	Gly	Leu	Glu	Leu	Leu	Ser	Asp	Met	Lys	Thr	Cys	Ile		
625				630					635						640		
Ile	Pro	Glu	Ala	Phe	Leu	Val	Phe	Thr	Ser	Arg	Ala	Thr	Ile	His	Arg		
			645						650					655			
Ile	Ser	Leu	Glu	Thr	Asn	Asn	Asn	Asp	Val	Ala	Ile	Pro	Leu	Thr	Gly		
			660					665					670				
Val	Lys	Glu	Ala	Ser	Ala	Leu	Asp	Phe	Asp	Val	Ser	Asn	Asn	His	Ile		
	675						680					685					
Tyr	Trp	Thr	Asp	Val	Ser	Leu	Lys	Thr	Ile	Ser	Arg	Ala	Phe	Met	Asn		
	690					695					700						
Gly	Ser	Ser	Val	Glu	His	Val	Ile	Glu	Phe	Gly	Leu	Asp	Tyr	Pro	Glu		
705				710					715						720		
Gly	Met	Ala	Val	Asp	Trp	Met	Gly	Lys	Asn	Leu	Tyr	Trp	Ala	Asp	Thr		
			725						730					735			
Gly	Thr	Asn	Arg	Ile	Glu	Val	Ala	Arg	Leu	Asp	Gly	Gln	Phe	Arg	Gln		
			740					745					750				
Val	Leu	Val	Trp	Arg	Asp	Leu	Asp	Asn	Pro	Arg	Ser	Leu	Ala	Leu	Asp		
		755					760					765					
Pro	Thr	Lys	Gly	Tyr	Ile	Tyr	Trp	Thr	Glu	Trp	Gly	Gly	Lys	Pro	Arg		
	770					775					780						
Ile	Val	Arg	Ala	Phe	Met	Asp	Gly	Thr	Asn	Cys	Met	Thr	Leu	Val	Asp		
785				790					795						800		
Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	Ala	Asp	Gln	Arg		
			805						810					815			
Leu	Tyr	Trp	Thr	Asp	Leu	Asp	Thr	Asn	Met	Ile	Glu	Ser	Ser	Asn	Met		
			820														

Asn Val Lys Ala Ile Asn Tyr Asp Pro Leu Asp Lys Phe Ile Tyr Trp  
 980 985 990  
 Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr Gln  
 995 1000 1005  
 Pro Ser Met Leu Thr Ser Pro Ser Gln Ser Leu Ser Pro Asp Arg Gln  
 1010 1015 1020  
 Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp Thr  
 1025 1030 1035 1040  
 Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu Asp Gly Asp Ala  
 1045 1050 1055  
 Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro Arg Ala Ile Ala  
 1060 1065 1070  
 Val Asn Ala Glu Arg Gly Tyr Met Tyr Phe Thr Asn Met Gln Asp His  
 1075 1080 1085  
 Ala Ala Lys Ile Glu Arg Ala Ser Leu Asp Gly Thr Glu Arg Glu Val  
 1090 1095 1100  
 Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu Val Val Asp Asn  
 1105 1110 1115 1120  
 Ala Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu Lys Arg Ile Glu  
 1125 1130 1135  
 Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu Glu Asp Ala Asn  
 1140 1145 1150  
 Ile Val Gln Pro Val Gly Leu Thr Val Leu Gly Arg His Leu Tyr Trp  
 1155 1160 1165  
 Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu Lys Thr Thr Gly  
 1170 1175 1180  
 Asp Lys Arg Thr Arg Val Gln Gly Arg Val Thr His Leu Thr Gly Ile  
 1185 1190 1195 1200  
 His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser Ala His Pro Cys  
 1205 1210 1215  
 Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile Ala Lys Gly Asp  
 1220 1225 1230  
 Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val Leu Leu Gln Asn  
 1235 1240 1245  
 Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro Asp Gln Phe Ala  
 1250 1255 1260  
 Cys Thr Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala Trp Arg Cys Asp  
 1265 1270 1275 1280  
 Gly Phe Pro Glu Cys Ala Asp Gln Ser Asp Glu Glu Gly Cys Pro Val  
 1285 1290 1295  
 Cys Ser Ala Ser Gln Phe Pro Cys Ala Arg Gly Gln Cys Val Asp Leu  
 1300 1305 1310  
 Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp Arg Ser Asp Glu  
 1315 1320 1325  
 Ala Asn Cys Asp Ala Val Cys Leu Pro Asn Gln Phe Arg Cys Thr Ser  
 1330 1335 1340  
 Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser Phe Pro Asp Cys  
 1345 1350 1355 1360  
 Ala Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Asn Lys Pro Pro Ser  
 1365 1370 1375  
 Asp Asp Ile Pro Ala His Ser Ser Ala Ile Gly Pro Val Ile Gly Ile  
 1380 1385 1390  
 Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe Val Cys Gln Arg  
 1395 1400 1405  
 Val Met Cys Gln Arg Tyr Thr Gly Ala Ser Gly Pro Phe Pro His Glu  
 1410 1415 1420  
 Tyr Val Gly Gly Ala Pro His Val Pro Leu Asn Phe Ile Ala Pro Gly  
 1425 1430 1435 1440  
 Gly Ser Gln His Gly Pro Phe Pro Gly Ile Pro Cys Ser Lys Ser Val  
 1445 1450 1455  
 Met Ser Ser Met Ser Leu Val Gly Gly Arg Gly Ser Val Pro Leu Tyr

	1460		1465		1470
Asp	Arg	Asn	His	Val	Thr
	1475		1480		1485
Lys	Ala	Thr	Leu	Tyr	Pro
	1490		1495		1500
Thr	Asp	Pro	Ser	Leu	Tyr
1505		1510		1515	
Pro	Ala	Thr	Ala	Arg	Pro
	1525		1530		1535
Pro	Pro	Thr	Thr	Pro	Cys
	1540		1545		1550
Ile	Ser	Arg	Trp	Lys	Ser
	1555		1560		1565
Ser	Asp	Pro	Tyr	Pro	Pro
1570		1575		1580	
Ala	Glu	Asp	Ser	Cys	Pro
1585		1590		1595	
His	Leu	Phe	Pro	Pro	Pro
	1605		1610		

<210> 3  
 <211> 200  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting vector

<400> 3  
 aaatatgcat tatcctgagc acagtgggtc tggcccttca cttggctgcc actcatggag 60  
 cctttatgct aaccacaggg gccaaccgcc tgaccctgga agatgccaac atcgtacagc 120  
 cagtaggtct gacagtgctg ggcaggcacc tctactggat cgaccgccag cagcagatga 180  
 tcgagcgtgt ggagaagacc 200

<210> 4  
 <211> 199  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting vector

<400> 4  
 tcactggcat ccatgcagtg aggaagtcag cctggaggag ttctgtacgt gagaggggac 60  
 agtgtttgtg gtggggtctc ctgggggaag gtgaatcagc cctactggca tcagatgggc 120  
 tgctggtgca agagcagtgt gcctgaggag ctcatgggct cagcaccgaa ggccagtgca 180  
 tgtccagatg tctgcctct 199